



1

PubMed	Nucleotide	Protein	Genome	Structure	Popset
Search	Find	Find	Find	Find	Find
Display	Default	View	HTML	Save	Add to Clipboard
					Hide Bar and Link Bar

☐ 1: GI = "7484807" [GenPept] AMP deaminase homolog F16M1... BLink, Related Sequences, Taxonomy

LOCUS T01259 600 aa PLN 14-MAY-1999  
 DEFINITION AMP deaminase homolog F16M14.21 - Arabidopsis thaliana.  
 ACCESSION T01259  
 PID g7484807  
 VERSION T01259 GI:7484807  
 DBSOURCE pir: locus T01259;  
 summary: #length 600 #molecular-weight 69656 #checksum 4877;  
 genetic: #map\_position 2 #introns 64/3; 82/1; 124/3; 184/3; 207/2;  
 255/1; 275/3; 313/3; 360/3; 411/3; 429/3; 466/3; 524/3; 551/3 #note  
 F16M14.21;  
 PIR dates: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change  
 14-May-1999.

KEYWORDS .  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 euphylllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core  
 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
 Arabidopsis.

REFERENCE 1 (residues 1 to 600)  
 AUTHORS Rounsley, S.D., Kaul, S., Lin, X., Ketchum, K.A., Crosby, M.L.,  
 Brandon, R.C., Sykes, S.M., Mason, T.M., Kerlavage, A.R., Adams, M.D.,  
 Somerville, C.R. and Venter, J.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (??-JUL-1998) to the EMBL Data Library

FEATURES Location/Qualifiers  
 source 1..600  
 /organism="Arabidopsis thaliana"  
 /db\_xref="taxon:3702"  
 Protein 1..600  
 /product="AMP deaminase homolog F16M14.21"

ORIGIN  
 1 miclevptsd eveaykclqe clelrkryvf qetvapweke visdpstpkp ntepfahypq  
 61 gksdhcfemq dgvvhvfank dakedlfpva datafftdlh hvlkviaagn irtlchrrlv  
 121 lleqkfnlhl mlnadkefla qksaphrdy nvrkvdthvh hsacmnqkhl lrfiksklrk  
 181 epdevvifrd gtyltlrevf esldltgydl nvdllldvhad kstfhrfdkf nlkynpcgqs  
 241 rlreiflkqd nliqgrflge itkqvfsdle askyqmaeyr isiygrkmse wdqlaswivn  
 301 ndlysenvvw liqlprlyni ykdmgivtsf qnildnifip lfeatvdpds hpqlhvfllkq  
 361 vvgfdldvde skperrptkh mptpaqwtna fnpafsyvy ycyanlyvln klreskgmtt  
 421 itlrphsgea gdidhlaatf ltchsiahi nlrkspvlqy lyllaqigla msplsnnsf  
 481 ldyhrnpfpv fflrglnvsl stddplqihl tkeplveeys iaasvwklsa cdlceiarns  
 541 vyqsgfshal kshwigkdy krgpdgndih ktnvphirve frdtvwneiy lfftqvnfsl  
 601

//